Press release – 26 May 2025

**Using bacteria to improve microbiota resistance to pathogens**

**INRAE scientists have identified seven bacteria involved in the microbiota barrier effect, which prevents pathogenic bacteria from proliferating. These findings, published in *Microbiome*, highlight the importance of the host microbiota composition in the success of a treatment based on beneficial bacteria.**

Antibiotic resistance is a major concern, particularly for immunocompromised patients, who are at greater risk of serious infections.

Microbiota composition can help prevent pathogenic bacteria from proliferating, which is known as the barrier effect. Targeted therapies are being developed to restore the microbiota by introducing beneficial bacteria.

In this study, INRAE scientists focused on one type of bacteria: vancomycin-resistant enterococci,[[1]](#footnote-1) or VRE. These bacteria are on a list established by the World Health Organization of six multidrug-resistant pathogens with priority status. The aim of this study was to identify the bacteria involved in the barrier effect and prove their effectiveness in preventing the proliferation of pathogenic bacteria, with a view to developing a therapeutic strategy.

Researchers took microbiota samples from mouse models that had been orally injected with enterococci. Using mathematical modelling, they identified seven bacteria out of more than 500 different species with a potential barrier effect: the more these bacteria were present, the fewer the pathogenic bacteria.

To prove the efficacy of these seven bacteria, the scientists compared mice treated with an antibiotic and infected with a VRE with and without administration of the bacterial mixture. The researchers found that the level of proliferation of pathogenic bacteria was lower with the addition of the bacterial mixture.

The efficacy of the bacterial mixture varied between the mice, which highlights the importance of the initial microbiota, as in humans. Laboratory experiments have shown that the seven bacteria alone could not inhibit the proliferation of pathogens in vitro, and initial results suggest that it is the combination of the bacterial mixture with the bacteria comprising the host microbiota that makes the treatment effective.

As well as working to improve our understanding of the anti-proliferative effects of bacteria and the associated mechanisms, the scientists’ next objective will be to gather a large repertoire of microorganisms from human microbiota to then consider applications in humans.

Based on a personalized medicine approach, the researchers are also working on predictive biomarkers. The process involves identifying different species of bacteria in a patient’s microbiota in order to estimate whether the bacterial treatment will work or to adapt it accordingly.

**Reference**

Jan A., Bayle P., Mohellibi N. et al. (2025). A consortium of seven commensal bacteria promotes gut microbiota recovery and strengthens ecological barrier against vancomycin-resistant enterococci. *Microbiome,* DOI: <https://doi.org/10.1186/s40168-025-02127-5>

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1. Vancomycin is used to treat certain severe infections caused by staphylococci or streptococci, or in patients allergic to beta-lactam antibiotics (penicillins or cephalosporins). [↑](#footnote-ref-1)